

10/525019

GIES3002.ST25  
SEQUENCE LISTING

<110> Giesing, Michael  
Suchy, Bernhard

<120> METHOD FOR ANALYZING BODY FLUIDS FOR THE PRESENCE OF CANCER  
CELLS, USE THEREOF, CORRESPONDING ANALYSIS KITS, AND USE OF  
SPECIFIC ACTIVE SUBSTANCES FOR TREATING CANCER

<130> GIES3002

<140> 10/525,019  
<141> 2005-02-18

<150> PCT/EP03/009229  
<151> 2003-08-20

<150> DE 102 38 046.5  
<151> 2002-08-20

<160> 22

<170> PatentIn version 3.3

<210> 1  
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<212> DNA  
<213> Artificial

<220>  
<223> forward primer (MNSOD)

<400> 1  
gtcaccgagg agaagtacca gg 22

<210> 2  
<211> 20  
<212> DNA  
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<220>  
<223> reverse primer (MNSOD)

<400> 2  
gggctgaggt ttgtccagaa 20

<210> 3  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> probe (MNSOD)

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cgttggccaa gggagatggt acagccc 27

<210> 4  
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<212> DNA  
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<220>  
<223> forward primer (TXNRD1)

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 acaaagtcca ggaccatcac ct 22

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 <211> 26  
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<220>  
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 ttgggctgcc tccttagcag ctgcca 26

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 <212> DNA  
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<220>  
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<400> 7  
 ctcggcttcc cgtgcaa 17

<210> 8  
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 <212> DNA  
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<220>  
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<400> 8  
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<210> 9  
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<220>  
 <223> probe (GPX1)

<400> 9  
 agtttgggca tcaggagaac gccaagaa 28

<210> 10  
 <211> 19  
 <212> DNA  
 <213> Artificial

GIES3002.ST25

<220>  
 <223> forward primer (GAPDH)  
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 <223> reverse primer (GAPDH)  
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 ggcagtgatg gcatggactg 20

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<210> 13  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens  
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Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala  
 1 5 10 15

Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Leu Pro Asp Leu Pro  
 20 25 30

Tyr Asp Tyr Gly Ala Leu Glu Pro His Ile Asn Ala Gln Ile Met Gln  
 35 40 45

Leu His His Ser Lys His His Ala Ala Tyr Val Asn Asn Leu Asn Val  
 50 55 60

Thr Glu Glu Lys Tyr Gln Glu Ala Leu Ala Lys Gly Asp Val Thr Ala  
 65 70 75 80

Gln Thr Ala Leu Gln Pro Ala Leu Lys Phe Asn Gly Gly Gly His Ile  
 85 90 95

Asn His Ser Ile Phe Trp Thr Asn Leu Ser Pro Asn Gly Gly Gly Glu  
 100 105 110

Pro Lys Gly Glu Leu Leu Glu Ala Ile Lys Arg Asp Phe Gly Ser Phe  
 Page 3

115

120

125

Asp Lys Phe Lys Glu Lys Leu Thr Ala Ala Ser Val Gly Val Gln Gly  
 130 135 140

Ser Gly Trp Gly Trp Leu Gly Phe Asn Lys Glu Arg Gly His Leu Gln  
 145 150 155 160

Ile Ala Ala Cys Pro Asn Gln Asp Pro Leu Gln Gly Thr Thr Gly Leu  
 165 170 175

Ile Pro Leu Leu Gly Ile Asp Val Trp Glu His Ala Tyr Tyr Leu Gln  
 180 185 190

Tyr Lys Asn Val Arg Pro Asp Tyr Leu Lys Ala Ile Trp Asn Val Ile  
 195 200 205

Asn Trp Glu Asn Val Thr Glu Arg Tyr Met Ala Cys Lys Lys  
 210 215 220

<210> 14  
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 <212> DNA  
 <213> Homo sapiens

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 cagcaggcag ctggctccgg ctttggggta tctgggctcc aggcagaagc acagcctccc 180  
 cgacctgccc tacgactacg gcgccttgga acctcacatc aacgcgcaga tcatgcagct 240  
 gcaccacagc aagcaccacg cggcctacgt gaacaacctg aacgtcaccg aggagaagta 300  
 ccaggaggcg ttggccaagg gagatgttac agcccagaca gctcttcagc ctgcactgaa 360  
 gttcaatggt ggtggtcata tcaatcatag cattttctgg acaaacctca gccctaacgg 420  
 tgggtggagaa cccaaagggg agttgctgga agccatcaaa cgtgactttg gttcctttga 480  
 caagttaaag gagaagctga cggctgcacg tgttgggtgct caaggctcag gttgggggtg 540  
 gcttggtttc aataaggaac ggggacactt acaaattgct gcttgtccaa atcaggatcc 600  
 actgcaagga acaacaggcc ttattccact gctggggatt gatgtgtggg agcacgctta 660  
 ctaccttcag tataaaaatg tcaggcctga ttatctaaaa gctatttgga atgtaatcaa 720  
 ctggggagaat gtaactgaaa gatacatggc ttgcaaaaag taaaccacga tcgttatgct 780  
 gagtatgtta agctctttat gactgttttt gtagtggtat agagtactgc agaatacagt 840  
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 atgctttgtg tgattg 976

GIES3002.ST25

<210> 15  
 <211> 497  
 <212> PRT  
 <213> Homo sapiens

<400> 15

Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr Asp Tyr Asp Leu Ile  
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Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala Ala Lys Glu Ala Ala  
 20 25 30

Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro  
 35 40 45

Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys  
 50 55 60

Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu  
 65 70 75 80

Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Thr Val Lys His  
 85 90 95

Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu  
 100 105 110

Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu  
 115 120 125

Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn  
 130 135 140

Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala  
 145 150 155 160

Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr  
 165 170 175

Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys  
 180 185 190

Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe  
 195 200 205

Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu  
 210 215 220

Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met  
 225 230 235 240

Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val

GIES3002.ST25  
250

245

255

Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln  
260 265 270

Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met  
275 280 285

Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr  
290 295 300

Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp  
305 310 315 320

Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu  
325 330 335

Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu  
340 345 350

Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu  
355 360 365

Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly  
370 375 380

Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu  
385 390 395 400

Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg  
405 410 415

Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn  
420 425 430

Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val  
435 440 445

Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln  
450 455 460

Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr  
465 470 475 480

Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly  
485 490 495

Cys

GIES3002.ST25

<211> 1314  
<212> DNA  
<213> Homo sapiens

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cggcctgccg gcggggacga cagcattgctg cctgggtgca gcagtgtgctg tctcggggaa 180  
gggaagatat ttttaaggcgt gtctgagcag acggggaggc ttttccaaac ccaggcagct 240  
tcgtggcgtg tgcggtttcg acccggtcac acaaagcttc agcatgtcat gtgaggacgg 300  
tcggggccctg aaaggaacgc tctcggaatt ggccgcggaa accgatctgc ccgttgtgtt 360  
tgtgaaacag agaaagatag gcggccatgg tccaaccttg aaggcttatc aggagggcag 420  
acttcaaaaag ctactaaaaa tgaacggccc tgaagatctt cccaagtcct atgactatga 480  
ccttatcatc attggaggtg gctcaggagg tctggcagct gctaaggagg cagcccaata 540  
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tcttgaggga acatgtgtga atgtgggttg catacctaaa aaactgatgc atcaagcagc 660  
tttgtttagga caagccctgc aagactctcg aaattatgga tggaaagtcg aggagacagt 720  
taagcatgat tgggacagaa tgatagaagc tgtacagaat cacattggct ctttgaattg 780  
gggctaccga gtagctctgc gggagaaaaa agtcgtctat gagaatgctt atgggcaatt 840  
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agagagtttt ctcattgcca ctggtgaaag accacgttac ttgggcatcc ctggtgacaa 960  
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caaaattggt gaacacatgg aagaacatgg catcaagttt ataagacagt tcgtaccaat 1200  
taaagttgaa caaattgaag cagggacacc aggccgactc agagtagtag ctcagtcac 1260  
caatagttag gaaatcattg aaggagaata taatacgggtg atgctggcaa tagg 1314

<210> 17  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 17

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1 5 10 15  
Phe Ser Ala Arg Pro Leu Ala Gly Gly Glu Pro Val Ser Leu Gly Ser  
20 25 30  
Leu Arg Gly Lys Val Leu Leu Ile Glu Asn Val Ala Ser Leu Cys Gly  
35 40 45

GIES3002.ST25

Thr Thr Val Arg Asp Tyr Thr Gln Met Asn Glu Leu Gln Arg Arg Leu  
50 55 60

Gly Pro Arg Gly Leu Val Val Leu Gly Phe Pro Cys Asn Gln Phe Gly  
65 70 75 80

His Gln Glu Asn Ala Lys Asn Glu Glu Ile Leu Asn Ser Leu Lys Tyr  
85 90 95

Val Arg Pro Gly Gly Gly Phe Glu Pro Asn Phe Met Leu Phe Glu Lys  
100 105 110

Cys Glu Val Asn Gly Ala Gly Ala His Pro Leu Phe Ala Phe Leu Arg  
115 120 125

Glu Ala Leu Pro Ala Pro Ser Asp Asp Ala Thr Ala Leu Met Thr Asp  
130 135 140

Pro Lys Leu Ile Thr Trp Ser Pro Val Cys Arg Asn Asp Val Ala Trp  
145 150 155 160

Asn Phe Glu Lys Phe Leu Val Gly Pro Asp Gly Val Pro Leu Arg Arg  
165 170 175

Tyr Ser Arg Arg Phe Gln Thr Ile Asp Ile Glu Pro Asp Ile Glu Ala  
180 185 190

Leu Leu Ser Gln Gly Pro Ser Cys Ala  
195 200

<210> 18  
<211> 856  
<212> DNA  
<213> Homo sapiens

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ctgtgagcct gggctccctg cggggcaagg tactacttat cgagaatgtg gcgtccctct 180  
gaggcaccac ggtccgggac tacaccaga tgaacgagct gcagcggcg ctcggacccc 240  
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GIES3002.ST25

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 tttcctctaa acctacgagg gaggaacacc ttgatcttac agaaaatacc acctcgagat 780  
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 agtgccgggt gtcagc 856

<210> 19  
 <211> 60  
 <212> DNA  
 <213> Artificial

<220>  
 <223> probe (NMSOD)

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<210> 20  
 <211> 60  
 <212> DNA  
 <213> Artificial

<220>  
 <223> probe (TXNRD1)

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<210> 21  
 <211> 60  
 <212> DNA  
 <213> Artificial

<220>  
 <223> probe (GPX2)

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<210> 22  
 <211> 60  
 <212> DNA  
 <213> Artificial

<220>  
 <223> probe (GPX3)

<400> 22  
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